

WEST Search History

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DATE: Tuesday, February 21, 2006

<u>Hide?</u>	<u>Set</u>	<u>Name</u>	<u>Query</u>	<u>Hit</u>	<u>Count</u>
<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>					
<input type="checkbox"/>	L1		(Pmepal or pmepla-1 or mivr1 or mivr-1) same (gene or sequence or \$1dna or protein or \$5peptide)		16

END OF SEARCH HISTORY



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1140558082-32062-97435568291.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
 3,743,317 sequences; 16,630,950,921 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

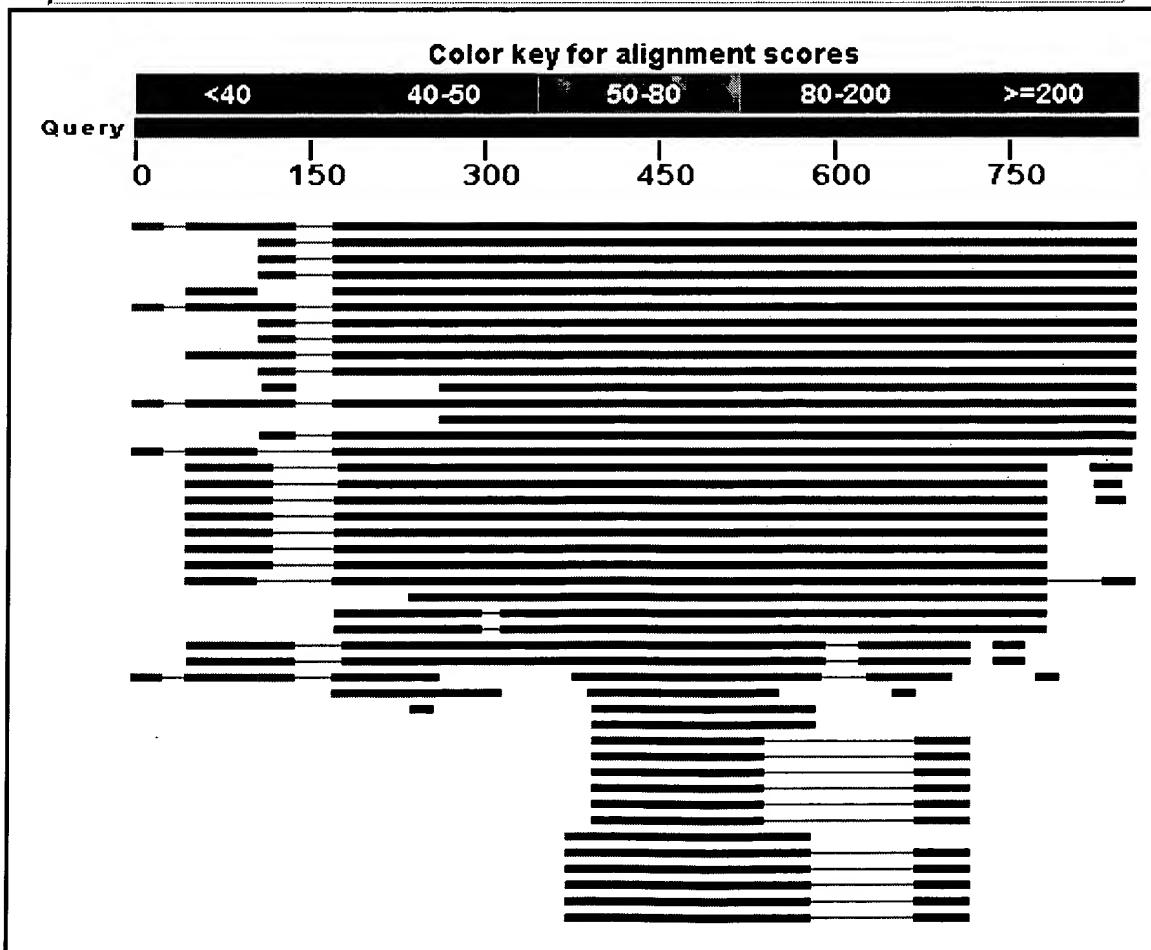
[Taxonomy reports](#)

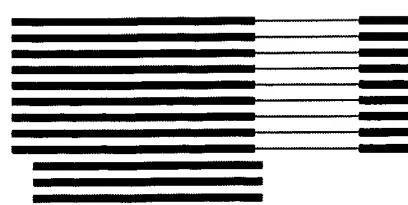
Query=

Length=861

Distribution of 140 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments





Sequences producing significant alignments:

			Score (Bits)	E Value
gi 40317614 ref NM_020182.3	Homo sapiens transmembrane, pros...	1322	0.0	
gi 40317615 ref NM_199169.1	Homo sapiens transmembrane, pros...	1322	0.0	
gi 40317619 ref NM_199171.1	Homo sapiens transmembrane, pros...	1322	0.0	
gi 40317617 ref NM_199170.1	Homo sapiens transmembrane, pros...	1322	0.0	
gi 50492890 emb CR612083.1	full-length cDNA clone CS0DJ015YF...	1322	0.0	
gi 16303741 gb AF305616.1 AF305616	Homo sapiens STAG1/PMEPA1 mRN	1322	0.0	
gi 22121998 gb AY128643.1	Homo sapiens PMEPA1 variant A protein	1322	0.0	
gi 9255808 gb AF224278.1 AF224278	Homo sapiens PMEPA1 protein (P	1322	0.0	
gi 16198474 gb BC015918.1	Homo sapiens transmembrane, prosta...	1314	0.0	
gi 51593770 gb BC080635.1	Homo sapiens transmembrane, prosta...	1298	0.0	
gi 11546043 emb AL035541.15 HS718J7	Human DNA sequence from c...	1039	0.0	
gi 15824468 gb AF305426.1 AF305426	Homo sapiens solid tumor-a...	1039	0.0	
gi 55652999 ref XM_514746.1	PREDICTED: Pan troglodytes LOC45836	995	0.0	
gi 73992626 ref XM_543070.2	PREDICTED: Canis familiaris simi...	872	0.0	
gi 82524234 emb CR956367.12	Pig DNA sequence from clone PigE...	644	0.0	
gi 18605637 gb BC023092.1	Mus musculus cDNA clone IMAGE:3989996	531	1e-147	
gi 23331176 gb BC036995.1	Mus musculus transmembrane, prosta...	531	1e-147	
gi 12843488 dbj AK008976.1	Mus musculus adult male stomach c...	529	5e-147	
gi 62027429 gb BC092094.1	Mus musculus cDNA clone IMAGE:3153171	529	5e-147	
gi 47124388 gb BC069890.1	Mus musculus transmembrane, prosta...	529	5e-147	
gi 31340603 ref NM_022995.2	Mus musculus transmembrane, pros...	529	5e-147	
gi 74201952 dbj AK136450.1	Mus musculus adult male colon cDN...	521	1e-144	
gi 62646459 ref XM_230899.3	PREDICTED: Rattus norvegicus tra...	464	2e-127	
gi 12004973 gb AF220208.1 AF220208	Mus musculus Nedd4 WW doma...	450	3e-123	
gi 82887825 ref XM_913670.1	PREDICTED: Mus musculus similar ...	424	2e-115	
gi 32398588 emb AL837509.11	Mouse DNA sequence from clone RP...	418	1e-113	
gi 53133895 emb AJ720618.1	Gallus gallus mRNA for hypothetical	303	5e-79	
gi 71895608 ref NM_001031492.1	Gallus gallus similar to Tran...	303	5e-79	
gi 7161781 emb AL121913.4 HSJ1059L7	Human DNA sequence from c...	182	1e-42	
gi 73945987 ref XM_541100.2	PREDICTED: Canis familiaris hypo...	178	2e-41	
gi 76651938 ref XM_588908.2	PREDICTED: Bos taurus hypothetical	168	2e-38	
gi 76633111 ref XM_869738.1	PREDICTED: Bos taurus similar to...	163	1e-36	
gi 68384134 ref XM_679680.1	PREDICTED: Danio rerio similar t...	157	7e-35	
gi 31790549 emb BX005347.5	Zebrafish DNA sequence from clone...	157	7e-35	
gi 34556291 gb AC111069.9	Mus musculus chromosome 18, clone ...	137	7e-29	
gi 26342572 dbj AK052338.1	Mus musculus 13 days embryo heart...	137	7e-29	
gi 26333688 dbj AK040289.1	Mus musculus 0 day neonate thymus...	137	7e-29	
gi 18490514 gb BC022716.1	Mus musculus DNA segment, Chr 18, ...	137	7e-29	
gi 31324574 ref NM_172631.2	Mus musculus DNA segment, Chr 18...	137	7e-29	
gi 66272338 gb BC096371.1	Mus musculus DNA segment, Chr 18, ...	137	7e-29	

gi 55647658 ref XM_512194.1 	PREDICTED: Pan troglodytes simil...	131	4e-27	
gi 22539691 gb BC030199.1 	Homo sapiens chromosome 18 open re...	131	4e-27	
gi 20455845 gb BC029958.1 	Homo sapiens chromosome 18 open re...	131	4e-27	
gi 51093709 ref NM_001003675.1 	Homo sapiens chromosome 18 op...	131	4e-27	
gi 51093707 ref NM_001003674.1 	Homo sapiens chromosome 18 op...	131	4e-27	
gi 51093712 ref NM_004338.2 	Homo sapiens chromosome 18 open ...	131	4e-27	
gi 51093722 ref NM_181483.2 	Homo sapiens chromosome 18 open ...	131	4e-27	
gi 51093715 ref NM_181482.2 	Homo sapiens chromosome 18 open ...	131	4e-27	
gi 51093725 ref NM_181481.2 	Homo sapiens chromosome 18 open ...	131	4e-27	
gi 16549670 dbj AK055028.1 	Homo sapiens cDNA FLJ30466 fis, c...	131	4e-27	
gi 2271474 gb AF009427.1 AF009427	Homo sapiens clone 22 mRNA,...	131	4e-27	
gi 2271472 gb AF009426.1 AF009426	Homo sapiens clone 22 mRNA,...	131	4e-27	
gi 2271470 gb AF009425.1 AF009425	Homo sapiens clone 22 mRNA,...	131	4e-27	
gi 2271468 gb AF009424.1 AF009424	Homo sapiens clone 22 mRNA,...	131	4e-27	
gi 21728137 dbj AP001010.4 	Homo sapiens genomic DNA, chromos...	131	4e-27	
gi 68444170 ref XM_694964.1 	PREDICTED: Danio rerio similar t...	123	1e-24	
gi 68392627 ref XM_686039.1 	PREDICTED: Danio rerio hypotheti...	123	1e-24	
gi 28144669 emb AL928820.8 	Zebrafish DNA sequence from clone...	123	1e-24	
gi 44890591 gb BC066971.1 	Homo sapiens chromosome 18 open re...	115	2e-22	
gi 53133395 emb AJ720368.1 	Gallus gallus mRNA for hypothetical	97.6	6e-17	
gi 71896400 ref NM_001031013.1 	Gallus gallus similar to Protein	97.6	6e-17	
gi 32398638 emb AL837520.26 	Mouse DNA sequence from clone RP...	85.7	2e-13	
gi 49900684 gb BC076211.1 	Danio rerio zgc:92731, mRNA (cDNA ...	71.9	3e-09	
gi 50540225 ref NM_001002580.1 	Danio rerio zgc:92731 (zgc:92731	71.9	3e-09	
gi 12860744 dbj AK020227.1 	Mus musculus 15 days embryo embry...	56.0	2e-04	
gi 61696641 gb AY803104.1 	Sus scrofa chromosome 17 clone pkmCon	48.1	0.047	
gi 58382298 ref XM_311847.2 	Anopheles gambiae str. PEST ENSA...	48.1	0.047	
gi 57968359 ref XM_563067.1 	Anopheles gambiae str. PEST ENSA...	48.1	0.047	
gi 77020632 gb AC155164.5 	Mus musculus BAC clone RP24-74L7 f...	42.1	2.9	
gi 44844522 emb BX088564.10 	Zebrafish DNA sequence from clon...	42.1	2.9	
gi 25046376 gb AC087063.20 	Mus musculus strain C57BL/6J clon...	42.1	2.9	
gi 86279771 gb CP000133.1 	Rhizobium etli CFN 42, complete genom	42.1	2.9	
gi 15873053 emb AJ328635.1 HSA328635	Homo sapiens genomic seq...	42.1	2.9	
gi 3337310 gb AC005284.1 AC005284	Homo sapiens chromosome 17,...	42.1	2.9	

Alignments

[Get selected sequences](#) [Select all](#) [Deselect all](#)

> [gi|40317614|ref|NM_020182.3|](#) **U E G** Homo sapiens transmembrane, prostate androger transcript variant 1, mRNA
Length=4930

Score = 1322 bits (667), Expect = 0.0
Identities = 688/688 (100%), Gaps = 0/688 (0%)
Strand=Plus/Plus

Query 174	CACGTGCCTGCTGAGCCACTACAAGCTGTCGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct 567	626
Query 234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct 627	686
Query 294	AGTGTCAAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCGCCTCGGCCACCACCGACCG	353

Sbjct	687	746
Query	354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	747	806
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTGCTGTCAGACGGGAGGAGCC	473
Sbjct	807	866
Query	474	CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTTGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	867	926
Query	534	GAACCGGGAGTCGGTGCAGCACCCCCAAACAGAACCATCTCGACAGTGACCTGATGGA	593
Sbjct	927	986
Query	594	TAGTGCCAGGCTGGCGGCCCTGnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTG	653
Sbjct	987	1046
Query	654	CTACGGCAGCGCGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTACGGCCA	713
Sbjct	1047	1106
Query	714	CTACCCGGGTCCCTCCAGCACCAGCAGCAGTGGCCGCCCTCCTGCTGGAGGG	773
Sbjct	1107	1166
Query	774	GACCCGGCTCCACCACACACACATCGGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	1167	1226
Query	834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct	1227	1254

Score = 188 bits (95), Expect = 2e-44

Identities = 95/95 (100%), Gaps = 0/95 (0%)

Strand=Plus/Plus

Query	47	GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTTTGTTCCAGAGCATGGAGA	106
Sbjct	440	499

Query	107	TCACGGAGCTGGAGTTGTTAGATCATCATCATC	141
Sbjct	500	534

Score = 56.0 bits (28), Expect = 2e-04

Identities = 28/28 (100%), Gaps = 0/28 (0%)

Strand=Plus/Plus

Query	1	ATGCACCGCTTGATGGGGTCAACAGCA	28
Sbjct	394	421

> gi|40317615|ref|NM_199169.1| UG Homo sapiens transmembrane, prostate androgen : transcript variant 2, mRNA
Length=4538

Score = 1322 bits (667), Expect = 0.0

Identities = 688/688 (100%), Gaps = 0/688 (0%)

Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTCATCAGCCGGCACAGCCA	233
Sbjct	175	234

Query	234	GGGGCGGAGGGAGAGAAGATGCCCTGTCCCTAGAAGGATGCCCTGGCCCTGGAGAGCAC	293
Sbjct	235	294

Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCGCCTGGCCCACCGACCG	353
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Sbjct	295	354
Query	354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	355	414
Query	414	GTACCTGCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	415	474
Query	474	CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	475	534
Query	534	GAACCGGGAGTCGGTGCAGCAGCAGACAGAACCATCTCGACAGTGACCTGATGGA	593
Sbjct	535	594
Query	594	TAGTGCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTG	653
Sbjct	595	654
Query	654	CTACGGCAGCGGCGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	655	714
Query	714	CTACCCGGGTCTCCTCCAGCACCAGCAGCAGTCAGGGCCGCCCTCCTGCTGGAGGG	773
Sbjct	715	774
Query	774	GACCCGGCTCCACCACACACATCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	775	834
Query	834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct	835	862

Score = 63.9 bits (32), Expect = 8e-07
 Identities = 32/32 (100%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query	110	CGGAGCTGGAGTTGTTAGATCATCATCATC	141
Sbjct	111	142

> gi|40317619|ref|NM_199171.1| UEG Homo sapiens transmembrane, prostate androgen transcript variant 4, mRNA
 Length=4590

Score = 1322 bits (667), Expect = 0.0
 Identities = 688/688 (100%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGCTGCACGGTCCTCATCAGCCGGCACAGCCA	233
Sbjct	227	286
Query	234	GGGGCGGAGAGAGAGATGCCCTGTCCTCAGAAGGATGCCCTGGCCCTCGGAGAGCAC	293
Sbjct	287	346
Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGAGGTCTACGCCCGCCTGGCCACCGACCG	353
Sbjct	347	406
Query	354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	407	466
Query	414	GTACCTGCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	467	526
Query	474	CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	527	586

Query 534	GAACCGGGAGTCGGTGCAGCAGCCAAACAGAACCATCTCGACAGTGACCTGATGGA	593
Sbjct 587	646
Query 594	TAGTGCAGGCTGGCGGCCCTGnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTG	653
Sbjct 647	706
Query 654	CTACGGCAGCGCGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct 707	766
Query 714	CTACCCGGGTCTCCTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTGCTGGAGGG	773
Sbjct 767	826
Query 774	GACCCGGCTCCACCAACACACATCGGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct 827	886
Query 834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct 887	914

Score = 63.9 bits (32), Expect = 8e-07
 Identities = 32/32 (100%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 110	CGGAGCTGGAGTTGTTCAAGATCATCATCATC	141
Sbjct 163	194

> gi|40317617|ref|NM_199170.1| U|G Homo sapiens transmembrane, prostate androgen : transcript variant 3, mRNA
 Length=4531

Score = 1322 bits (667), Expect = 0.0
 Identities = 688/688 (100%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query 174	CACGTGCCTGCTGAGCCACTACAAGCTGTCAGCAGGCCACAGCCA	233
Sbjct 168	227
Query 234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGCCCTCGGAGAGCAC	293
Sbjct 228	287
Query 294	AGTGTCAAGCAACGGAATCCCAGAGCCGAGGTCTACGCCCGCCTGGCCCACCGACCG	353
Sbjct 288	347
Query 354	CCTGGCCGTGCCGCCCTCGCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct 348	407
Query 414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGAGGAGCC	473
Sbjct 408	467
Query 474	CCCACCTACCAGGGCCCTGCACCCCTCAGCTTGGACCCGAGCAGCAGCTGGAAC	533
Sbjct 468	527
Query 534	GAACCGGGAGTCGGTGCAGCAGCCAAACAGAACCATCTCGACAGTGACCTGATGGA	593
Sbjct 528	587
Query 594	TAGTGCAGGCTGGCGGCCCTGnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTG	653
Sbjct 588	647
Query 654	CTACGGCAGCGCGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct 648	707
Query 714	CTACCCGGGTCTCCTCCAGCACCAAGCAGCAGCAGTGGGCCGCCCTCCTGCTGGAGGG	773
Sbjct 708	767

Query 774 GACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA 833
 Sbjct 768 827

Query 834 GAAGGATAAACAGAAAGGACACCCCTCTC 861
 Sbjct 828 855

Score = 63.9 bits (32), Expect = 8e-07
 Identities = 32/32 (100%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 110 CGGAGCTGGAGTTGTTCAGATCATCATCATC 141
 Sbjct 104 135

> gi|50492890|emb|CR612083.1| U full-length cDNA clone CS0DJ015YF12 of T cells (J1
 Cot 10-normalized of Homo sapiens (human)
 Length=901

Score = 1322 bits (667), Expect = 0.0
 Identities = 688/688 (100%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query 174 CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGCCTTCATCAGCCGGCACAGCCA 233
 Sbjct 6 65

Query 234 GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC 293
 Sbjct 66 125

Query 294 AGTGTCAAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCG 353
 Sbjct 126 185

Query 354 CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC 413
 Sbjct 186 245

Query 414 GTACCTGCAGCACGAGATGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC 473
 Sbjct 246 305

Query 474 CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTTGGACCCCGAGCAGCAGCTGGAAC 533
 Sbjct 306 365

Query 534 GAACCGGGAGTCGGTGCAGCACCCCCAACAGAACCATTTGACAGTGACCTGATGGA 593
 Sbjct 366 425

Query 594 TAGTGCCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGCATCAGGCCACGTG 653
 Sbjct 426 485

Query 654 CTACGGCAGCGGGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTACGGCCA 713
 Sbjct 486 545

Query 714 CTACCCGGGTCCCTCCTCCAGCACCAGCAGAGCAGTGGCCGCCCTTGCTGGAGGG 773
 Sbjct 546 605

Query 774 GACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA 833
 Sbjct 606 665

Query 834 GAAGGATAAACAGAAAGGACACCCCTCTC 861
 Sbjct 666 693

> gi|16303741|gb|AF305616.1|AF305616 U E G Homo sapiens STAG1/PMEPA1 mRNA, comple
 Length=4839

Score = 1322 bits (667), Expect = 0.0
 Identities = 688/688 (100%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query 174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct 494	553
Query 234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTGGAGAGCAC	293
Sbjct 554	613
Query 294	AGTGTCAAGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCGCTCGGCCACCGACCG	353
Sbjct 614	673
Query 354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct 674	733
Query 414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct 734	793
Query 474	CCCACCCCTACCAGGGCCCTGCACCCCTCAGCTTCGGGACCCCGAGCAGCAGCTGGA	533
Sbjct 794	853
Query 534	GAACCGGGAGTCGGTGCAGCAGCCCCAACAGAACCATCTTCGACAGTGACCTGATGGA	593
Sbjct 854	913
Query 594	TAGTGCCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGCATCAGGCCACGTG	653
Sbjct 914	973
Query 654	CTACGGCAGCGGCGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTACCGGCCA	713
Sbjct 974	1033
Query 714	CTACCCGGGTCCCTCCTCCAGCACAGCAGAGCAGTGGCCGCCCTCCTGCTGGAGGG	773
Sbjct 1034	1093
Query 774	GACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct 1094	1153
Query 834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct 1154	1181

Score = 188 bits (95), Expect = 2e-44
 Identities = 95/95 (100%), Gaps = 0/95 (0%)
 Strand=Plus/Plus

Query 47	GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTTTGTTCCAGAGCATGGAGA	106
Sbjct 367	426
Query 107	TCACGGAGCTGGAGTTGTTCAAGATCATCATCATC	141
Sbjct 427	461

Score = 56.0 bits (28), Expect = 2e-04
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query 1	ATGCACCGCTTGATGGGGTCAACAGCA	28
Sbjct 321	348

> gi|22121998|gb|AY128643.1| UEG Homo sapiens PMEPA1 variant A protein mRNA, cor Length=1818

Score = 1322 bits (667), Expect = 0.0
 Identities = 688/688 (100%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGCTGCACGGTCCTCATCAGCCGGCACAGCCA	233
Sbjct	168	227
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	228	287
Query	294	AGTGTCAAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCACCGACCG	353
Sbjct	288	347
Query	354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGGCCACCTATCC	413
Sbjct	348	407
Query	414	GTACCTGCAGCACGAGATGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct	408	467
Query	474	CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	468	527
Query	534	GAACCGGGAGTCGGTGCAGCAGCCCCAAACAGAACCATTTGACAGTGACCTGATGGA	593
Sbjct	528	587
Query	594	TAGTGCCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACTCGGCATCAGGCCACGTG	653
Sbjct	588	647
Query	654	CTACGGCAGCGGGCGCATGGAGGGCGCCGCCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct	648	707
Query	714	CTACCCGGGTCCCTCCTCCAGCACAGCAGCAGTCAGGGCCGCCCTCCTGCTGGAGGG	773
Sbjct	708	767
Query	774	GACCCGGCTCCACCACACACATCGCGCCCTAGAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	768	827
Query	834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct	828	855

Score = 63.9 bits (32), Expect = 8e-07
 Identities = 32/32 (100%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query	110	CGGAGCTGGAGTTGTTAGATCATCATCATC	141
Sbjct	104	135

>gi|9255808|gb|AF224278.1|AF224278 UEG Homo sapiens PMEPA1 protein (PMEPA1) mRNA
 Length=1141

Score = 1322 bits (667), Expect = 0.0
 Identities = 688/688 (100%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGCTGCACGGTCCTCATCAGCCGGCACAGCCA	233
Sbjct	164	223
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	224	283
Query	294	AGTGTCAAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCACCGACCG	353
Sbjct	284	343

Query 354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct 344	403
Query 414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct 404	463
Query 474	CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTCGGGACCCGAGCAGCAGCTGGAACCT	533
Sbjct 464	523
Query 534	GAACCGGGAGTCGGTGCAGCACCCAAACAGAACCATCTCGACAGTGACCTGATGGA	593
Sbjct 524	583
Query 594	TAGTGCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACCTGGGCATCGGCCACGTG	653
Sbjct 584	643
Query 654	CTACGGCAGCGCGGGCGCATGGAGGGCCGCCCACCTACAGCGAGGTCATCGGCCA	713
Sbjct 644	703
Query 714	CTACCCGGGTCTCCTCCAGCACCAAGCAGAGCAGTGGCCGCCCTCCTGCTGGAGGG	773
Sbjct 704	763
Query 774	GACCCGGCTCCACCACACACATCGGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct 764	823
Query 834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct 824	851

Score = 63.9 bits (32), Expect = 8e-07
 Identities = 32/32 (100%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 110	CGGAGCTGGAGTTGTTAGATCATCATCATC	141
Sbjct 100	131

> gi|16198474|gb|BC015918.1| UEG Homo sapiens transmembrane, prostate androgen : (cDNA clone IMAGE:4559576), partial cds
 Length=1061

Score = 1314 bits (663), Expect = 0.0
 Identities = 687/688 (99%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query 174	CACGTGCCTGCTGAGCCACTACAAGCTGTCACGGCTTCATCAGCCGGCACAGCCA	233
Sbjct 154	213
Query 234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct 214	273
Query 294	AGTGTCAAGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCGCCTCGGCCACCGACCG	353
Sbjct 274	333
Query 354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct 334	393
Query 414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC	473
Sbjct 394G.....	453
Query 474	CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTCGGGACCCGAGCAGCAGCTGGAACCT	533
Sbjct 454	513
Query 534	GAACCGGGAGTCGGTGCAGCACCCAAACAGAACCATCTCGACAGTGACCTGATGGA	593

Sbjct	514	573
Query	594	TAGTGCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACCTGGCATCAGGCCACGTG	653
Sbjct	574	633
Query	654	CTACGGCAGCGCGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTACGGCCA	713
Sbjct	634	693
Query	714	CTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGCCGCCCTCCTGCTGGAGGG	773
Sbjct	694	753
Query	774	GACCCGGCTCCACCACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	754	813
Query	834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct	814	841

Score = 188 bits (95), Expect = 2e-44
 Identities = 95/95 (100%), Gaps = 0/95 (0%)
 Strand=Plus/Plus

Query	47	GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTTTGTTCCAGAGCATGGAGA	106
Sbjct	27	86
Query	107	TCACGGAGCTGGAGTTGTTAGATCATCATCATC	141
Sbjct	87	121

> gi|51593770|gb|BC080635.1| **UIG** Homo sapiens transmembrane, prostate androgen invariant 2, mRNA (cDNA clone MGC:99523 IMAGE:6569922), complete cds
 Length=1060

Score = 1298 bits (655), Expect = 0.0
 Identities = 685/688 (99%), Gaps = 0/688 (0%)
 Strand=Plus/Plus

Query	174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct	153T.....	212
Query	234	GGGGCGGAGGAGAGAAGATGCCCTGTCCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC	293
Sbjct	213	272
Query	294	AGTGTCAAGCAACGGAATCCCAGAGCCGAGGTCTACGCCCCGCCCTGGCCCACCGACCG	353
Sbjct	273	332
Query	354	CCTGGCCGTGCCGCCCTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC	413
Sbjct	333	392
Query	414	GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGCC	473
Sbjct	393G.....G.....	452
Query	474	CCCACCCCTACCAGGGCCCTGCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAC	533
Sbjct	453	512
Query	534	GAACCGGGAGTCGGTGCAGCAGGAAACAGAACCATTTGACAGTGACCTGATGGA	593
Sbjct	513	572
Query	594	TAGTGCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACCTGGCATCAGGCCACGTG	653
Sbjct	573	632
Query	654	CTACGGCAGCGGGCGCATGGAGGGCCGCCACCTACAGCGAGGTACGGCCA	713
Sbjct	633	692

Query	714	CTACCCGGGGTCCCTCCTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTGCTGGAGGG	773
Sbjct	693	752
Query	774	GACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGA	833
Sbjct	753	812
Query	834	GAAGGATAAACAGAAAGGACACCCCTCTC	861
Sbjct	813	840

Score = 63.9 bits (32), Expect = 8e-07
 Identities = 32/32 (100%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query	110	CGGAGCTGGAGTTGTTCAGATCATCATCATC	141
Sbjct	89	120

> [gi|11546043|emb|AL035541.15|HS718J7](#) **EID** Human DNA sequence from clone RP4-718J7
 Contains the PCK1 gene for soluble phosphoenolpyruvate
 carboxykinase 1, the ZBP1 gene for Z-DNA binding protein
 1, the 3' end of the TMEPAI gene for transmembrane prostate
 androgen induced mRNA, two putative novel genes, the 5' end
 of the CTCFL gene for CCCTC-binding factor (zinc finger)-like
 and a CpG island, complete sequence
 Length=130435

Score = 1039 bits (524), Expect = 0.0
 Identities = 545/545 (100%), Gaps = 0/545 (0%)
 Strand=Plus/Minus

Query	317	AGCCGCAGGTCTACGCCCGCCTGGCCCACCGACCGCCTGGCCGTGCCGCCCTCGCCC	376
Sbjct	128443	128384
Query	377	AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACC	436
Sbjct	128383	128324
Query	437	TGCCACCCACCATCTGCTGTCAAGACGGGAGGGAGCCCCACCCCTACCAAGGGCCCTGCA	496
Sbjct	128323	128264
Query	497	CCCTCCAGCTTGGGACCCCGAGCAGCAGCTGGAACGTGAACCGGGAGTCGGTGGCGCAC	556
Sbjct	128263	128204
Query	557	CCCCAACAGAACCATCTCGACAGTGACCTGATGGATAGTGCCAGGCTGGCGGCCCT	616
Sbjct	128203	128144
Query	617	GnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTGCTACGGCAGCGGGGGCATGG	676
Sbjct	128143	128084
Query	677	AGGGGCCGCCACCTACAGCGAGGTACGGCCACTACCCGGGTCCTCCAGC	736
Sbjct	128083	128024
Query	737	ACCAGCAGAGCAGTGGCCGCCCTCCTGCTGGAGGGACCCGGCTCCACACACACA	796
Sbjct	128023	127964
Query	797	TCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACC	856
Sbjct	127963	127904
Query	857	CTCTC 861	
Sbjct	127903 127899	

Score = 107 bits (54), Expect = 6e-20

Identities = 54/54 (100%), Gaps = 0/54 (0%)
 Strand=Plus/Minus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAAGGAAACGGAATCCCAGAG 318
 Sbjct 128929 128876

> gi|15824468|gb|AF305426.1|AF305426 D Homo sapiens solid tumor-associated 1 protein gene, complete cds
 Length=61505

Score = 1039 bits (524), Expect = 0.0
 Identities = 545/545 (100%), Gaps = 0/545 (0%)
 Strand=Plus/Plus

Query 317 AGCCGCAGGTCTACGCCCGCCTCGGCCACCGACCGCCTGGCGTGGCCGCCCTCGCCC 376
 Sbjct 57303 57362

Query 377 AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACC 436
 Sbjct 57363 57422

Query 437 TGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCACCCCTACCAAGGGCCCTGCA 496
 Sbjct 57423 57482

Query 497 CCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACGTGAACCGGGAGTCGGTGCGCGAC 556
 Sbjct 57483 57542

Query 557 CCCCAAACAGAACCATCTCGACAGTGACCTGATGGATAGTGCAGGCTGGCGGCCCT 616
 Sbjct 57543 57602

Query 617 GnnnnnnnAGCAGTAACCTCGGCATCAGGCCACGTGCTACGGCAGCGGGGGCGCATGG 676
 Sbjct 57603 57662

Query 677 AGGGGCCGCCGCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTCCAGC 736
 Sbjct 57663 57722

Query 737 ACCAGCAGAGCAGTGGCCGCCCTCCTGCTGGAGGGACCCGGCTCCACACACACACA 796
 Sbjct 57723 57782

Query 797 TCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACC 856
 Sbjct 57783 57842

Query 857 CTCTC 861
 Sbjct 57843 57847

Score = 182 bits (92), Expect = 1e-42
 Identities = 92/92 (100%), Gaps = 0/92 (0%)
 Strand=Plus/Plus

Query 174 CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA 233
 Sbjct 50270 50329

Query 234 GGGCGGGAGGAGAGAAGATGCCCTGTCCCTCAG 265
 Sbjct 50330 50361

Score = 125 bits (63), Expect = 3e-25
 Identities = 63/63 (100%), Gaps = 0/63 (0%)
 Strand=Plus/Plus

Query 47 GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTTTGTTCCAGAGCATGGAGA 106
 Sbjct 367 426

Query 107 TCA 109
 Sbjct 427 ... 429

Score = 107 bits (54), Expect = 6e-20
 Identities = 54/54 (100%), Gaps = 0/54 (0%)
 Strand=Plus/Plus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAAGGAAACGGAATCCCAGAG 318
 Sbjct 56817 56870

Score = 63.9 bits (32), Expect = 8e-07
 Identities = 32/32 (100%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 110 CGGAGCTGGAGTTGTTCAGATCATCATCATC 141
 Sbjct 50206 50237

Score = 56.0 bits (28), Expect = 2e-04
 Identities = 28/28 (100%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query 1 ATGCACCGCTTGTGGGGTCAACAGCA 28
 Sbjct 321 348

> [gi|55652999|ref|XM_514746.1|](#) G PREDICTED: Pan troglodytes LOC458363 (LOC458363), Length=1059

Score = 995 bits (502), Expect = 0.0
 Identities = 538/543 (99%), Gaps = 0/543 (0%)
 Strand=Plus/Plus

Query 319 CCGCAGGTCTACGCCCGCCTCGGCCACCGACCGCCCTGGCCGTGCCGCCCTCGCCAG 378
 Sbjct 454 513

Query 379 CGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTG 438
 Sbjct 514 C 573

Query 439 CCACCCACCATCTCGCTGTCAAGACGGGGAGGGAGCCCCACCCCTACCAAGGGCCCCTGCACC 498
 Sbjct 574 ..G.....G..... 633

Query 499 CTCCAGCTTCGGGACCCCGAGCAGCAGCTGAACTGAACCGGGAGTCGGTGCACCC 558
 Sbjct 634 693

Query 559 CCAAACAGAACCATCTCGACAGTGACCTGATGGATAGTGCCAGGCTGGCGGCCCTGn 618
 Sbjct 694 753

Query 619 nnnnnnAGCAGTAACCTGGGCATCAGCGCCACGTGCTACGGCAGCGCGGGCGCATGGAG 678
 Sbjct 754 813

Query 679 GGGCCGCCGCCACCTACAGCGAGGTACCGCCACTACCCGGGGCTCCCTCCAGCAC 738
 Sbjct 814 A 873

Query 739 CAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGACCCGGCTCCACACACACATC 798
 Sbjct 874 933

Query 799 GCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCC 858
 Sbjct 934 C 993

Query 859 CTC 861
 Sbjct 994 ... 996

Score = 107 bits (54), Expect = 6e-20
 Identities = 54/54 (100%), Gaps = 0/54 (0%)
 Strand=Plus/Plus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAAGAACGGAATCCCAGAG 318
 Sbjct 294 347

> gi|73992626|ref|XM_543070.2| G PREDICTED: Canis familiaris similar to Transmembrane androgen-induced protein (Solid tumor-associated 1 protein) (LOC485945), mRNA
 Length=2142

Score = 872 bits (440), Expect = 0.0
 Identities = 634/691 (91%), Gaps = 3/691 (0%)
 Strand=Plus/Plus

Query 174 CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA 233
 Sbjct 471G..C.....G..... 530

Query 234 GGGGC GGAGGAGAGAAGATGCCCTGTCCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCAC 293
 Sbjct 531 ...CA.....G.....C.....G..... 590

Query 294 AGTGTCAAGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCGCCTCGGCCAACCGACCG 353
 Sbjct 591 G.....G.....T.....T..GA..... 650

Query 354 CCTGGCCGTGCCGCCCTCGCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC 413
 Sbjct 651C.....A.....C.....C.. 710

Query 414 GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGAGGAGCC 473
 Sbjct 711C.....G.....G..... 770

Query 474 CCCAC CCTACCAGGGCCCTGCACCCCTCCAGCTTGGGACCCCGAGCAGCAGCTGGAAC 533
 Sbjct 771 ...G.....G.....G.....G.. 830

Query 534 GAACCGGGAGTCGGTGC CGCACCCCCAAACAGAACCATCTCGACAGTGACCTGATGGA 593
 Sbjct 831C.....G.....G.....C..... 890

Query 594 TAGTGCCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTG 653
 Sbjct 891 C.....T.T..... 950

Query 654 CTACGGCAGCGGGCGGCATGGAGGGCCGCCACCTACAGCGAGGTACCGGCCA 713
 Sbjct 951GG.....T.....C..... 1010

Query 714 CTACCCGGGTCC---TCCTTCCAGCACCAGCAGAGCAGTGGCCGCCCTTGCTGGA 770
 Sbjct 1011CCGG.....C..... 1070

Query 771 GGGGACCCGGCTCCACCAACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAA 830
 Sbjct 1071C.....G.....C.....G.....A.....TGC..... 1130

Query 831 AGAGAAGGGATAAACAGAAAGGACACCCCTCTC 861
 Sbjct 1131 ...A.....C.....G..... 1161

Score = 44.1 bits (22), Expect = 0.73
 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Plus

Query 112 GAGCTGGAGTTGTTCA GATCATCATCATC 141
 Sbjct 409G.....C..... 438

> gi|82524234|emb|CR956367.12| D Pig DNA sequence from clone PigE-122C21 on chromosome 12
Length=124577

Score = 644 bits (325), Expect = 0.0
Identities = 494/544 (90%), Gaps = 3/544 (0%)
Strand=Plus/Minus

Query 317	AGCCGCAGGTCTACGCCCGCCTGGCCACCGACCGCCTGGCGTGGCCGCCCTCGCCC	376
Sbjct 55054C.....G.....G.....C.....	54995
Query 377	AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCGTACCTGCAGCACGAGATCGACC	436
Sbjct 54994C.....C.....	54935
Query 437	TGCCACCCACCATCTCGCTGTCAGACGGGAGGAGCCCCCACCTACCAGGGCCCTGCA	496
Sbjct 54934G.....G.....C.....G.....G.....G.....	54875
Query 497	CCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACGTGAACCGGGAGTCGGTGCGCGCAC	556
Sbjct 54874	.G.....G.....G.....C.....G.....	54815
Query 557	CCCCAACAGAACCATCTCGACAGTGACCTGATGGATAGTGCCAGGCTGGCGGCCCT	616
Sbjct 54814G.....C.....C..C....T.....	54755
Query 617	GnnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTGCTACGGCAGCGGGCGGCGATGG	676
Sbjct 54754	.T.....GG.....	54695
Query 677	AGGGGCCGCCGCCACCTACAGCGAGGTACGGCCACTACCCGG---GTCCTCCTTCC	733
Sbjct 54694C.....C.....G.....C..CGCC...A.....	54635
Query 734	AGCACCAAGCAGAGCAGTGGGCCCTCCTGCTGGAGGGACCCGGCTCCACCAACACAC	793
Sbjct 54634C..C.....G.....C.G...G.....	54575
Query 794	ACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGAC	853
Sbjct 54574C..G..A.G..GGC..G.....G..C..	54515
Query 854	ACCC 857	
Sbjct 54514 54511	

Score = 125 bits (63), Expect = 3e-25
Identities = 63/63 (100%), Gaps = 0/63 (0%)
Strand=Plus/Minus

Query 47	GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTTTGTTCCAGAGCATGGAGA	106
Sbjct 104963	104904
Query 107	TCA 109	
Sbjct 104903	... 104901	

Score = 91.7 bits (46), Expect = 3e-15
Identities = 79/90 (87%), Gaps = 0/90 (0%)
Strand=Plus/Minus

Query 174	CACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCA	233
Sbjct 59532C..T..C.....C..G.....	59473
Query 234	GGGGCGGAGGAGAGAAGATGCCCTGTCCTC 263	
Sbjct 59472	...CA..C....G.....C..G.....	59443

Score = 60.0 bits (30), Expect = 1e-05
Identities = 48/54 (88%), Gaps = 0/54 (0%)
Strand=Plus/Minus

Query 265 GAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAAGGAAACGGAATCCCAGAG 318
 Sbjct 55548C.....G.....G.....GT.....G..... 55495

Score = 48.1 bits (24), Expect = 0.047
 Identities = 27/28 (96%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

Query 1 ATGCACCGCTTGTGGGGTCAACAGCA 28
 Sbjct 105009A..... 104982

> gi|18605637|gb|BC023092.1| UEG Mus musculus cDNA clone IMAGE:3989996, partial Length=1079

Score = 531 bits (268), Expect = 1e-147
 Identities = 528/608 (86%), Gaps = 12/608 (1%)
 Strand=Plus/Plus

Query 178 TGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGG 237
 Sbjct 188A..C..C.....A.....CC 247

Query 238 CGGAGGAGAGAAGATGCCCTGTCCCTCAGAAGGATGCCCTGTGGCCCTCGGAGAGCACAGTG 297
 Sbjct 248 A.....C....GA.....G.....C.....A.....T..G... 307

Query 298 TCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCGCCTCGGCCAACCGACCGCCTG 357
 Sbjct 308T---.G..G.....A.....T.....T.....A..C 364

Query 358 GCCGTGCCGCCCTCGCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTAC 417
 Sbjct 365 ..T.....C.....AT.....-.....A.....A.....C..C... 415

Query 418 CTGCAGCACGAGATCGACCTGCCACCCACCATCTGCTGTCAAGACGGGAGGGAGCCCCA 477
 Sbjct 416A..T.C.....A.....A.....T..T..... 475

Query 478 CCCTACCAGGGCCCTGCACCCCTCAGCTCGGACCCCGAGCAGCAGCTGGAACCTGAAC 537
 Sbjct 476A.....T.....A.....G..... 535

Query 538 CGGGAGTCGGTGC CGC CACCCCAAACAGAACCATCTCGACAGTGACCTGATGGATAGT 597
 Sbjct 536A..T.....T..C.G.....T..A..C..C 595

Query 598 GCCAGGCTGGCGGCCCTGnnnnnnnnAGCAGTAACCTGGGCATCAGGCCACGTGCTAC 657
 Sbjct 596 A...T.....G.....T.....C..... 655

Query 658 GGCAGCGCGGGCGCATGGAGGGGCCCGCCACCTACAGCGAGGTACCGCCACTAC 717
 Sbjct 656 A.....T.....C..... 715

Query 718 CCGGGGTCCCTCCAGCACAGCAGAGCAGTGGGCCGCCCTCCTGCTGGAGGGGACC 777
 Sbjct 716 ..T..C.....A..T.AC.....AT.....C....A..... 775

Query 778 CGGCTCCA 785
 Sbjct 776 783

Score = 111 bits (56), Expect = 4e-21
 Identities = 71/76 (93%), Gaps = 0/76 (0%)
 Strand=Plus/Plus

Query 47 GGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTTTGTTCCAGAGCATGGAGA 106
 Sbjct 57G.....C.G.....CC..... 116

Query 107 TCACGGAGCTGGAGTT 122
 Sbjct 117 132